

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 12:43:17 ; Search time 3 Seconds  
(without alignments)  
5.539 Million cell updates/sec

Title: US-10-035-958-60

Perfect score: 890  
Sequence: 1 AAGTACTGTGTCTCGGGTGG.....TAAATAAAATCATCAAA 890

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 12 seqs, 9336 residues

Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 12 summaries

Database : k035rng:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	865.7	97.3	909	AACT7539	Human ORFX ORF3094
2	858.9	96.5	903	AAAI5582	Human phospholipid
3	858.9	96.5	903	ADR70378	Respiratory disease
4	858.3	96.4	897	AAFP94490	Human hydrophobic
5	784.3	88.1	826	AAK97660	Extended human sec
6	784.3	88.1	826	AAK42252	Human phosphatidyl
7	664.7	74.7	681	AAFP94480	Human hydrophobic
8	167.2	18.8	303	AAK62175	Porcine muscular s
9	120.2	13.5	133	AAH85783	Human single nucle
10	49.4001	5.6	686	ABR09032	Phase-1 Rat CT gen
11	48.8	5.5	1078	AAD42238	Corn FT homologue
12	48.2	5.4	1191	AAD42243	Corn FT homologue

# ALIGNMENTS

RESULT 1  
AACT7539  
ID AACT7539 standard; cDNA, 909 BP.  
XX  
XX  
AC AACT7539;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF3094 polynucleotide sequence SEQ ID NO:6187.  
XX  
XX Human; open reading frame; ORFX; detection; cytosolic; hepatocytic;  
XX vulnery; antiparietic; antiparkinsonian; neurotropic; neuroprotective;  
XX anticonvulsant; osteopathic; antirheumatic; immunosuppressant; cardian;  
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
XX hypotensive; dermatological; immunosuppressive; antineoplastic;  
XX antiviral; antibacterial; antifungal; antineumatic; antithyroid;

KW	antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW	cholesterol ester storage; systemic lupus erythematosus; infection;
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW	bone damage; cartilage damage; antineoplastic disease; coagulation;
KW	thrombosis; contraceptive; ss.
OS	Homo sapiens.
XX	
XX	WO200058473-A2.
PN	
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000MO-US008621.
XX	
PR	31-MAR-1999; 99US-0127607P.
PR	02-APR-1999; 99US-0127636P.
PR	05-APR-1999; 99US-0127728P.
PR	30-MAR-2000; 2000US-00540763.
XX	
PA	(CUBA-) CUBAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
DR	WPI; 2000-602362/57.
DR	P-PSDB; AAB43330.
XX	
PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders,
PT	neurodegenerative disorders and cardiovascular disease.
PS	Claim 5; Page 5369-5370; 5507pp; English.
XX	
CC	AACT74446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC	sequences have activities such as: cytosolic; hepatocytic; vulnery;
CC	antiparietic; antiparkinsonian; neurotropic; neuroprotective; osteopathic;
CC	anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;
CC	cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC	dermatological; immunosuppressive; antineoplastic; antibacterial;
CC	antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
CC	sequences can be used for determining the presence of or predisposition
CC	to, or preventing or treating pathological conditions associated with an
CC	ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC	proteins in gene therapy vectors. The proteins and nucleic acids may be
CC	used to treat cancers, proliferative disorders, neurodegenerative
CC	disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC	diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC	storage, systemic lupus erythematosus, severe combined immunodeficiency
CC	(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC	disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC	cartilage damage, nocturnal haemoglobinuria, antineoplastic disease; to
CC	enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX	
XX	Sequence 909 BP; 232 A; 254 C; 236 G; 186 T; 0 U; 1 Other;
XX	
QY	Query Match 97.3%; Score 865.7; DB 1; Length 909;
QY	Best Local Similarity 99.0%; Pred. No. 0;
QY	Matches 881; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Db	
QY	1 AAGTACTGTGTCTCGGGTGGTGAATGCTGGCGAGCCCTGGAAGCTGCTGCTCC 60
Db	12 AAGTACTGTGTCTCGGGTGGTGAATGCTGGCGAGCCCTGGAAGCTGCTTTC 71
QY	61 TTCTCCCTGCTTAAACAGAGAGTCCCAATGAGCTTGAATGAGCTTGAACAGCAGC 120
Db	72 TTCTCCCTGCTTAAACAGAGAGTCCCAATGAGCTTGAATGAGCTTGAACAGCAGC 131
QY	121 ACTGTTACTGGTCTCAATGATGCTGCTCACTGGAACAGAGATGGAACAGCCCGTGTCC 180
Db	132 ACTGTTACTGGTCTCAATGATGCTGCTCACTGGAACAGAGATGGAACAGCCCGTGTCC 191

```

QY 181 CCATGAGGCCCTTGGACGAGACACCTCTTTTGGCAGGGCTTGAAGTTTCTAACCC 240
Db 192 CCATGAGGCCCTTGGACGAGACACCTCTTTTGGCAGGGCTTGAAGTTTCTAACCC 251
QY 241 AGAGTTGGGGAACATTGGCTGCAAGTTGTTCTGATTGTAACTACAGACAGAGAT 300
Db 252 AGAGTTGGGGAACATTGGCTGCAAGTTGTTCTGATTGTAACTACAGACAGAGAT 311
QY 301 CACCTCTGATGAGAGCCGATGATCAAGTTCCCGGGGGCCGAGAGAGCCGACCTATAT 360
Db 312 CACCTCTGATGAGAGCCGATGATCAAGTTCCCGGGGGCCGAGAGAGCCGACCTATAT 371
QY 361 CCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 372 CCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
QY 421 ACATTGGCTGTAAAGATATCAAGAGCCGACCTGTAAGAAAGGAGATTCAAGGCCA 480
Db 432 ACATTGGCTGTAAAGATATCAAGAGCCGACCTGTAAGAAAGGAGATTCAAGGCCA 491
QY 481 GGAATTATGAGCTTACAGAGCTCCCTCCGACCGGACACAGTGGCTTCAATGCTACCA 540
Db 492 GGAATTATGAGCTTACAGAGCTCCCTCCGACCGGACACAGTGGCTTCAATGCTACCA 551
QY 541 GTTCTTTGCTATCTTCAAGAAAGAAAGTCAATCTCTCTCTCCAGAAAGAAACAAAC 600
Db 552 GTTCTTTGCTATCTTCAAGAAAGAAAGTCAATCTCTCTCTCCAGAAAGAAACAAAC 611
QY 601 TCGAGGCTCTTGAAGAAATGACAGATTTGTAACCGCTTCCACTGGGGGAAACCTGAAGC 660
Db 612 TCGAGGCTCTTGAAGAAATGACAGATTTGTAACCGCTTCCACTGGGGGAAACCTGAAGC 671
QY 661 AAGCAACCACTTCAATGACAGCCAGAACTACAGAGCTACCAACCTTCCAGAGCTCCAGAG 720
Db 672 AAGCAACCACTTCAATGACAGCCAGAACTACAGAGCTACCAACCTTCCAGAGCTCCAGAG 731
QY 721 AAGGCGCAGCGAGCCCAAGCC-AAAACGAGCAGAGATAGTGGCTCTGATAGCCGG 779
Db 732 AAGGCGCAGCGAGCCCAAGC-AAAACGAGCAGAGATAGTGGCTCTGATAGCCGG 791
QY 780 CTTTGCATCCGGGATGAGCCAGACAGTCTCAACCAAGAGATGAGTGAAGCCG 839
Db 792 CTTTGCATCCGGGATGAGCCAGACAGTCTCAACCAAGAGATGAGTGAAGCCG 851
QY 840 CTTGAGATACGAACCCCTTCTTTTCAAAATTAATAAATAATCATCA 889
Db 852 CTTGAGATACGAACCCCTTCTTTTCAAAATTAATAAATAATCATCA 901

```

RESULT 2  
 AAA15582  
 ID AAA15582 standard; cDNA, 903 BP.

XX AAA15582;

XX 01-AUG-2000 (first entry)

XX Human phospholipid binding protein 2, PLBP2 gene.

XX Human, phospholipid binding protein, PLBP2; foetal development disorder;  
 KW reproduction disorder; cell proliferation disorder; immune response;  
 KW autoimmune disorder; AIDS; infertility; cytoskeletal; immunosuppressive;  
 KW gene therapy; hereditary neuropathy;  
 KW phosphatidylethanolamine binding protein D1; PE-BP D1; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 88..771

XX FT /\*tag= a

XX FT /product= "Human PLBP2"

```

PN US603767-A.
XX 16-MAY-2000.
PD 09-DEC-1998; 98US-00208718.
XX 28-OCT-1997; 97US-00958820.
XX (INCY-) INCYTE PHARM INC.
XX Corley NC, Shah P, Lal P, Hillman JL;
XX WPI: 2000-375529/32.
XX P-PSDB: AAY94263.
DR New purified phospholipid binding proteins 1 and 2 useful for diagnosing,
PT treating or preventing diseases disorders associated with fetal
PT development, reproduction, cell proliferation, and the immune response.
PS Example 5; Fig 2; 37bp, English.
XX The present sequence is the phospholipid binding protein 2 (PLBP2) gene.
CC This gene is expressed in lung, prostate and heart tissues. Also, the
CC protein is expressed in foetal tumour tissues. PLBP2 may be used for the
CC diagnosis, prevention, or treatment of disorders associated with foetal
CC development (e.g. hereditary neuropathies), reproduction (e.g.
CC infertility), cell proliferation (e.g. cancers), and the immune response
CC (AIDS). PLBP2 antibodies may also be developed for potential drug
CC screening or to quantitate PLBP2 gene expression in biopsied tissues. The
CC PLBP2 gene may be administered for gene therapy of disorders associated
CC with PLBP2. PLBP2 has high homology with the phosphatidylethanolamine
CC binding protein D1, PE-BP D1, of Onchocerca volvulus. PE-BP D1 is thought
CC to play a role in transport or signal mechanisms between membranes and
CC the cytoplasm
XX SQ
Sequence 903 BP; 222 A; 251 C; 242 G; 188 T; 0 U; 0 Other;
Query Match 96.5%; Score 858.9; DB 1; Length 903;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 2 AGTACTTGTCTCCGGGTGTGACTGATTAAGTGGAGCCCTGGAAGCTGCTTCT 61
Db 1 AGTACTTGTCTCCGGGTGTGACTGATTAAGTGGAGCCCTGGAAGCTGCTTCT 60
QY 62 TCTCCGCTTAACACAGAGTGGCCATGGGTGGACATAGAGCTGTACAGACGA 121
Db 61 TCTCCGCTTAACACAGAGTGGCCATGGGTGGACATAGAGCTGTACAGACGA 120
QY 122 CTGTACTGGGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
Db 121 CTGTACTGGGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 182 CATGAGCCCTCTTGGACAGACACCTCTTTTGGCAGAGGCTTGAAGTTTCAACCA 241
Db 181 CATGAGCCCTCTTGGACAGACACCTCTTTTGGCAGAGGCTTGAAGTTTCAACCA 240
QY 242 GAGTTGGGGAACATTGGCTGCAAGGTTTCTGATTGTAACATCAAGAGAGATC 301
Db 241 GAGTTGGGGAACATTGGCTGCAAGGTTTCTGATTGTAACATCAAGAGAGATC 300
QY 302 ACCTCTGATGAGAGCCGATGATCAAGTTCCCGGGGGCCGTGAGAGCGGCACTATATC 361
Db 301 ACCTCTGATGAGAGCCGATGATCAAGTTCCCGGGGGCCGTGAGAGCGGCACTATATC 360
QY 362 CTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
Db 361 CTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 422 CATGGCTGTAAAGATATCAAGAGCCGACCTGTAAGAAAGGAGATTCAAGGCCAG 481
Db 421 CATGGCTGTAAAGATATCAAGAGCCGACCTGTAAGAAAGGAGATTCAAGGCCAG 480

```



XX AAP94490;  
AC  
XX  
XX  
DT 04-JUN-2001 (first entry)  
XX  
XX  
DE Human hydrophobic domain containing protein clone HP03880 cDNA #114.  
XX  
XX  
KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;  
KW antianaemic; vulnery; antilux; osteopathic; anti-inflammatory;  
KW cytosolic; gene therapy; autoimmune disorder; multiple sclerosis;  
KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing  
KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;  
KW behavioural characteristic; immune response; ss.  
XX  
OS Homo sapiens.  
XX  
PN M0200112660-A2.  
XX  
PN 22-FEB-2001.  
XX  
PD 10-AUG-2000; 2000MO-JP005356.  
PF  
PR 17-AUG-1999; 99JP-00230344.  
PR 07-SEP-1999; 99JP-00252551.  
PR 01-OCT-1999; 99JP-00281132.  
PR 22-OCT-1999; 99JP-00301624.  
PR 04-NOV-1999; 99JP-00313877.  
XX  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
PI  
PI Kato S, Kimura T;  
XX  
XX MPI; 2001-160059/16.  
XX P-PSDB; AAB88590.  
XX  
XX  
PT Human proteins with hydrophobic domains and the DNAs which encode them  
PT are useful for treating autoimmune disorders, burns and tumors and for  
PT screening novel pharmaceuticals.  
XX  
XX  
PS Claim 4; Page 442-444; 518pp; English.  
XX  
XX AAP94417 to AAP94516 encode the human proteins given in AAB88557 to  
CC AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,  
CC anti-HIV, neuroprotective, antianaemic, vulnery, antilux,  
CC osteopathic, anti-inflammatory and cytosolic activities, and can be used  
CC in gene therapy. (I) can be used as pharmaceuticals and as antigens to  
CC prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes  
CC for genetic diagnosis and gene sources for gene therapy or for producing  
CC (I) in large quantities. Cells containing (II) are used for the detection  
CC of ligands or receptors corresponding to membrane or secretory proteins  
CC and to screen small molecule novel pharmaceuticals. Antibodies directed  
CC to (I) can be used for the detection, quantification and purification of  
CC (I). Activities of (I) may include cytokine and cell  
CC proliferation/differentiation function, immune stimulating or suppressing  
CC activity, haematopoiesis regulating activity, tissue growth activity,  
CC activin/inhibin activity, retractor/ligand activity and anti-inflammatory  
CC and thrombolytic activity. receptor/ligand activity and anti-inflammatory  
CC activity. (I) and (II) can be used to treat autoimmune disorders e.g.  
CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,  
CC inflammatory bowel disease and tumours. (I) and (II) can also be used for  
CC wound healing, as nutritional sources or supplements e.g. as amino acid,  
CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,  
CC processing and utilisation of dietary fat, protein, carbohydrate, to affect  
CC vitamins and minerals, to effect behavioural characteristics, to affect  
CC appetite, and can act as antigens in vaccines to raise an immune response  
CC to the protein or another material cross-reactive with the protein  
XX  
XX Sequence 897 BP; 226 A; 253 C; 224 G; 184 T; 0 U; 0 Other;

Qy	1	AAGTACTGTGTCGCGGTGTGAGATAGATTAAGCTGTGGAGCCCTGGAAAGCTCTGTGCC	6
Db	11	AAGTACTGTGTGTCGCGGTGTGAGATAGATTAAGCTGTGGAGCCCTGGAAAGCTCTGTGCC	7
Qy	61	TTCTCCCTGTGCTTAACCAAGAGTGCCCATGGTGTGACAAATGAGGTGGTCAACAGAC	12
Db	71	TTCTCCCTGTGCTTAACCAAGAGTGCCCATGGTGTGACAAATGAGGTGGTCAACAGAC	13
Qy	121	ACTGTACTGGGTCTCAATGATGTGTGTCACTGTGAGAGAGAGATGTAGAAACAGCCGTGTGC	18
Db	131	ACTGTACTGGGTCTCAATGATGTGTGTCACTGTGAGAGAGAGATGTAGAAACAGCCGTGTGC	19
Qy	181	CCATGAGGCCCTCTTGGACGAGAGCAACCTCTTTTTCGACAGGCGCTTGAAGTTTTCACCC	24
Db	191	CCATGAGGCCCTCTTGGACGAGAGCAACCTCTTTTTCGACAGGCGCTTGAAGTTTTCACCC	25
Qy	241	AGAGTTGGGGAAACATTGGCTGCAAGGTGTTCTGTATGTTTACAACTTACAGACAGAGAT	30
Db	251	AGAGTTGGGGAAACATTGGCTGCAAGGTGTTCTGTATGTTTACAACTTACAGACAGAGAT	31
Qy	301	CACCTCTGTGATGAGCCGATAGTCAAGTTCGCCGGGGCGCGTGTGACGCGCAACCTATAT	36
Db	311	CACCTCTGTGATGAGCCGATAGTCAAGTTCGCCGGGGCGCGTGTGACGCGCAACCTATAT	37
Qy	361	CCTGGTATGTGTGATCCAGATGTGCTCTGACAGAGCAAAACCCAGACAGAGATTTCTGAG	42
Db	371	CCTGGTATGTGTGATCCAGATGTGCTCTGACAGAGCAAAACCCAGACAGAGATTTCTGAG	43
Qy	421	ACATTGGCTGTATCAATATTCAGAGGCGCGCATCTGAGAAAGGGAAGATTACAGGGGCA	48
Db	431	ACATTGGCTGTATCAATATTCAGAGGCGCGCATCTGAGAAAGGGAAGATTACAGGGGCA	49
Qy	481	GGAGTTATCAAGCCTTACCAAGGCTCCCTCCCAACCGGCAACAAGTGGCTTCAATGCTTACA	54
Db	491	GGAGTTATCAAGCCTTACCAAGGCTCCCTCCCAACCGGCAACAAGTGGCTTCAATGCTTACA	55
Qy	541	GTTCTTTGTCTATCTTCAGAGAGAAAGTCACTCTCTCTCTTCCGACAGAAACCAAAAC	60
Db	551	GTTCTTTGTCTATCTTCAGAGAGAAAGTCACTCTCTCTCTTCCGACAGAAACCAAAAC	61
Qy	601	TCGAGGCTCTTGGAAAAATGACAGATTTTGTAAACCGCTTCAACTGTGGCGAACTGTAGAC	66
Db	611	TCGAGGCTCTTGGAAAAATGACAGATTTTGTAAACCGCTTCAACTGTGGCGAACTGTAGAC	67
Qy	661	AAGCACCAGTTCATGACCCAGAACTACACGAGCTCAACAACCTCCAGAGTCCCAAGAG	72
Db	671	AAGCACCAGTTCATGACCCAGAACTACACGAGCTCAACAACCTCCAGAGTCCCAAGAG	73
Qy	721	AAGGGCCAGGAGGCCCAAGCAC-AAAACAGGCMAGATAGCTGCTGTAGATAGCCGG	77
Db	731	AAGGGCCAGGAGGCCCAAGCACAAAACAGGCGAGATAGCTGCTGTAGATAGCCGG	79
Qy	780	CTTTGGCAATCGGGCATGTGGCACTGTCTCAACAACGAGATGTGGATGTGAAACCCC	83
Db	791	CTTTGGCAATCGGGCATGTGGCAACTGTGCCCAACAACGAGATGTGGATGTGAAACCCC	85
Qy	840	CTCTGGATTCAGAAACCCCTTCTTTTCCAAATTAAAAAAA 880	
Db	851	CTCTGGATTCAGAAACCCCTTCTTTTCCAAATMAAAAAAAA 891	
RESULT 5			
AAK97660			
ID AAK97660 standard; DNA; 826 BP.			
XX AAK97660;			
AC			
DT 13-SEP-1999 (first entry)			
XX			
DE Extended human secreted protein coding sequence, SEQ ID NO. 124.			
XX			
TM Secreted protein; human; cytokine; cellular proliferation; cell movement;			

KW cellular differentiation; immune system regulator; anti-inflammatory;  
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
 KW genetic disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9931236-A2.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 17-DEC-1998; 98WO-1B002122.  
 XX  
 PR 17-DEC-1997; 97US-0069957P.  
 PR 09-FEB-1998; 98US-0074121P.  
 PR 13-APR-1998; 98US-0081563P.  
 PR 10-AUG-1998; 98US-0096116P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Bouquelieret L, Duclert A, Dumas Milne Edwards J;  
 XX  
 DR WPI: 1999-385906/32.  
 DR P-PSDB; AAY35976.  
 XX  
 PT New isolated human secreted proteins.  
 XX  
 PS Claim 1; Page 255; 516pp; English.  
 XX  
 CC This sequence represents an extended human secreted protein coding  
 CC sequence of the invention. The secreted proteins can be used in treating  
 CC or controlling a variety of human conditions. The secreted proteins may  
 CC act as cytokines or may affect cellular proliferation or differentiation  
 CC or may act as immune system regulators, haematopoiesis regulators, tissue  
 CC growth regulators, regulators of reproductive hormones or cell movement  
 CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or  
 CC tumour inhibitory activity. The DNAs can be used in forensic procedures  
 CC to identify individuals or in diagnostic procedures to identify  
 CC individuals having genetic diseases resulting from abnormal expression of  
 CC the genes corresponding to the extended cDNAs. They are also useful for  
 CC constructing a high resolution map of the human chromosomes. They can  
 CC also be used for gene therapy to control or treat genetic diseases  
 CC  
 CC  
 SQ Sequence 826 BP; 228 A; 229 C; 211 G; 158 T; 0 U; 0 Other;

Query Match 88.1%; Score 784.3; DB 1; Length 826;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 799; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 75 AACCAAGAGTGCCTGATGGTGGACAATGAGGCTGTGACAGAGACATGTTACTGGATC 134  
 DB 1 AACCAAGAGTGCCTGATGGTGGACAATGAGGCTGTGACAGAGACATGTTACTGGATC 60  
 QY 135 TCATGATGTTGCTGCTGCTGAGAGACGAGAGATGAGAAACGCCGTGTGCCATGAGGCCCTCT 194  
 DB 61 TCATGATGTTGCTGCTGCTGAGAGACGAGAGATGAGAAACGCCGTGTGCCATGAGGCCCTCT 120  
 QY 195 TGGACGAGAGACACCCCTTTTGGCAGGCGCTTGAATTTTCTACCCAGAGTTGGGGAAACA 254  
 DB 121 TGGACGAGAGACACCCCTTTTGGCAGGCGCTTGAATTTTCTACCCAGAGTTGGGGAAACA 180  
 QY 255 TTGGCTGCAAGGTTGTTCTGATTTGAACAATACTACAGACAGAGATCACCTCTGGATG 314  
 DB 181 TTGGCTGCAAGGTTGTTCTGATTTGAACAATACTACAGACAGAGATCACCTCTGGATG 240  
 QY 315 AGCGATAGTCAAGTTCCCGGGGGCGGTGACGCGCAACTATATCTGTGTAGTGTG 374  
 DB 241 AGCGATAGTCAAGTTCCCGGGGGCGGTGACGCGCAACTATATCTGTGTAGTGTG 300  
 QY 375 ATCCAGATGCCCCCTACAGAGCAAGCAACAGAGATTTCTGAGACATTTGGCTGTAA 434  
 DB 301 ATCCAGATGCCCCCTACAGAGCAAGCAACAGAGATTTCTGAGACATTTGGCTGTAA 360

QY 435 CAGATATCAAGGCGCGCGACCTTGAAGAAAGGAAAGATTTCAGGCGCAGAGATTACGCT 494  
 DB 361 CAGATATCAAGGCGCGCGCGACCTTGAAGAAAGGAAAGATTTCAGGCGCAGAGATTACGCT 420  
 QY 495 ACCAGGCTCCCTCCCGACCGGACACAGTGGCTTCATGGCTTACACGTTCTTTGTATAC 554  
 DB 421 ACCAGGCTCCCTCCCGACCGGACACAGTGGCTTCATGGCTTACACGTTCTTTGTATAC 480  
 QY 555 TTCAGGAAGAAAGTCAATCTCTCTCTCCCAAGGAAACAAACCTCAGAGCTTTGGA 614  
 DB 481 TTCAGGAAGAAAGTCAATCTCTCTCTCCCAAGGAAACAAACCTCAGAGCTTTGGA 540  
 QY 615 AATGACAGATTTTGAACCGCTTTCACCTGCGGCAACCTGAAAGACACCACTTCA 674  
 DB 541 AATGACAGATTTTGAACCGCTTTCACCTGCGGCAACCTGAAAGACACCACTTCA 600  
 QY 675 TGACCCAGAACTTACAGAGACTACCAACCTCTCCAGGCTCCAGAGAAAGGCGCAGAGC 734  
 DB 601 TGACCCAGAACTTACAGAGACTACCAACCTCTCCAGGCTCCAGAGAAAGGCGCAGAGC 660  
 QY 735 CCAAGCAC-AAAACAGAGAGATAGCTGCTGTAGATTAGCGGCTTTGCCATCCGG 793  
 DB 661 CCAAGCACAAAACAGAGAGATAGCTGCTGTAGATTAGCGGCTTTGCCATCCGG 720  
 QY 794 CATGTGGCCACACTGCTCAACAACGAGTGTGGTATGAAACCCCTTGTGATACAGAA 853  
 DB 721 CATGTGGCCACACTGCTCAACAACGAGTGTGGTATGAAACCCCTTGTGATACAGAA 780  
 QY 854 CCCCTTCTTTTCCAAATTAATAAAAAA 880  
 DB 781 CCCCTTCTTTTCCAAATTAATAAAAAA 807

RESULT 5  
 AA242252  
 ID AA242252 standard; cDNA; 826 BP.  
 XX  
 AC AA242252;  
 XX  
 DT 01-FEB-2000 (first entry)  
 XX  
 XX Human phosphatidylethanolamine-binding protein encoding cDNA.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;  
 KW gene therapy; chromosome mapping; upstream regulatory sequence; forensic;  
 KW location; development; protein synthesis; stability; regulation;  
 KW identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9933051-A2.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 09-APR-1999; 99WO-1B000712.  
 XX  
 PR 09-APR-1998; 98US-00057719.  
 PR 28-APR-1998; 98US-00069047.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI: 2000-038446/03.  
 DR P-PSDB; AAY64647.  
 XX  
 PT Novel secreted protein 5' expressed sequence tag sequences used in  
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures.  
 XX  
 PS Example 21; Page 168-169; 837pp; English.  
 XX  
 CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)  
 CC sequences, corresponding to human secreted proteins. AAY64651 to AAY65438

CC represents the EST-related proteins corresponding to AA42265 to AA43052. CC The 5' ESTs can be used for producing secreted human gene products. They CC can be used to identify and isolate 5' untranslated regions (UTRs) and CC upstream regulatory regions which control the location, development CC stage, rate, and quantity of protein synthesis, as well as stability of CC mRNA. The ESTs are also useful as probes for chromosome mapping, and to CC obtain full length cDNA clones. The ESTs can also be used in forensic CC procedures to identify individuals, or in diagnostic procedures to CC identify individuals having genetic diseases resulting from abnormal gene CC expression. The products may also be used in gene therapy protocols. The CC nucleic acids encoding signal peptides can be used for directing CC extracellular secretion of a polypeptide or the insertion of a CC polypeptide into a membrane, or importing a polypeptide into a cell. The CC proteins encoded by the EST sequences may be useful in treating a variety CC of human conditions. Secreted proteins have therapeutic value, and the CC identification of new secreted proteins is valuable. AA42265 to AA43264 CC and AA46644 to AA46450 represent sequences used in the exemplification CC of the present invention

Sequence 826 BP; 228 A; 229 C; 211 G; 158 T; 0 U; 0 Other;

Query Match	88.1%;	Score 784.3;	DB 1;	Length 826;
Best Local Similarity	99.0%;	Pred. No. 0;		
Matches 799;	Conservative 0;	Mismatches 7.	Indels 1.	Cons 1

QY	75	AACGAGAGTGGCCATGGGTTTGACAATGAGCGTGGTCAACGAGACGTTTAACTGGAGTC	134
Db	1	AACGAGAGTGGCCATGGGTTTGACAATGAGCGTGGTCAACGAGACGTTTAACTGGAGTC	60
QY	135	TCATGATGGTGGTCACTGGAGACGAGGATGAGAAACGCCGTGTGCCCATTGAGGCCCTTC	194
Db	61	TCATGATGGTGGTCACTGGAGACGAGGATGAGAAACGCCGTGTGCCCATTGAGGCCCTTC	120
QY	195	TGAGACAGGACACCCCTCTTTTGGCAGAGGCGCTTGAAGTTTCTACCAAGATTGGGAAACA	254
Db	121	TGAGACAGGACACCCCTCTTTTGGCAGAGGCGCTTGAAGTTTCTACCAAGATTGGGAAACA	180
QY	255	TTGGCTGCAAGGTTGTTCTCTGAATTGTATCAACTACAGACAGAAAGATCACTTCGTGATGG	314
Db	181	TTGGCTGCAAGGTTGTTCTCTGAATTGTATCAACTACAGACAGAAAGATCACTTCGTGATGG	240
QY	315	AGCCGATATCAAGTTCCCGGGGGCCGTGACGGCGCAACTATATCTCTGTGATGTGG	374
Db	241	AGCCGATATCAAGTTCCCGGGGGCCGTGACGGCGCAACTATATCTCTGTGATGTGG	300
QY	375	ATCCAGATGCCCTCTAGACAGACAGAACCCAGACAGATTCGTGAGACATTTGGCTGTGTA	434
Db	301	ATCCAGATGCCCTCTAGACAGACAGAACCCAGACAGATTCGTGAGACATTTGGCTGTGTA	360
QY	435	CAGATATCAAGGGCCGCCGACTGAAGAAAGGAAAGATTCAAGGCGCAGAGATTATCAGCCT	494
Db	361	CAGATATCAAGGGCCGCCGACTGAAGAAAGGAAAGATTCAAGGCGCAGAGATTATCAGCCT	420
QY	495	ACGAGGTCCTCCCTCCCAACCGGACACAGATGGCTTCATCGCTACCAAGTTCTTTGTCTATC	554
Db	421	ACGAGGTCCTCCCTCCCAACCGGACACAGATGGCTTCATCGCTACCAAGTTCTTTGTCTATC	480
QY	555	TTCAGGAAGAAAGTCACTCTCTCTCTTCCCAAGAAAAACAATCTCGAGGCTCTTGGAA	614
Db	481	TTCAGGAAGAAAGTCACTCTCTCTCTTCCCAAGAAAAACAATCTCGAGGCTCTTGGAA	540
QY	615	AAATGGAAGAATTTCTGAAACCGCTTCCACTCGGCGCAACTGAAAGCAAGCAACCAAGTTCA	674
Db	541	AAATGGAAGAATTTCTGAAACCGCTTCCACTCGGCGCAACTGAAAGCAAGCAACCAAGTTCA	600
QY	675	TGACCCAGAACTACAGAGACTCAACCAACCTCCAGGCTCCCAAGAGAAAGGCGCAAGGAGC	734
Db	601	TGACCCAGAACTACAGAGACTCAACCAACCTCCAGGCTCCCAAGAGAAAGGCGCAAGGAGC	660
QY	735	CCAAGGAC-AAAACCAAGCAGAGATAGCTGCTGTGATAGCCGAGCTTTGGCCATCGGAG	793
Db	661	CCAAGGACAAAAAACCAAGCGGAGATAGCTGCTGTGATAGCCGAGCTTTGGCCATCGGAG	720

QY	79	CAATGGCCACACTGTCTACCAACCGACGATGTGGTATGAAACCCCTCTGGATACAGAA	85
DB	721	CATGTGGCCACTGTGCCACCAACGACGATGTGGTATGAAACCCCTCTGGATACAGAA	780
QY	854	CCCCCTCTTTTCCAAATTAAAAAAA	880
DB	781	CCCCCTCTTTTCCAAATTAAAAAAA	807

RESULT 7  
A8E94400

ID	AAF94480 standard; cDNA; 681 BP
YY	

AAF94480 ;

DT 04-JUN-2001 (first entry)  
xx

DE Human hydrophobic domain containing protein clone HP03880 cDNA #104.  
XX

KM human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;  
KM antineoplastic; vunerary; antitumor; osteopathic; anti-inflammatory;  
KM cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;  
KM HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing  
KM inflammatory bowel disease; nutritional supplement; appetite; vaccine;  
KM behavioural characteristic; immune response; ss.

OS Homo sapiens.

PN WO200112660-A2.

PD 22-FEB-2001.

PF 10-AUG-2000; 2000WO-JP005356.

PR 17-AUG-1999; 99JP-00230344.  
PR 07-SEP-1999; 99JP-00252551.  
PR 01-OCT-1999; 99JP-00281132.  
PR 22-OCT-1999; 99JP-00301624.  
PR 04-NOV-1999; 99JP-00313877.

PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
PA

PI Kato S, Kimura T;  
.....

DR WPI; 2001-160059/16.  
DR P-PSDB; AAB88590.

Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for screening novel pharmaceuticals.

Claim 3; Page 426-427; 518pp; English.

AA8949417 (I) AAF94516 encode the human protein given in AA888557 to AA888606 (I) which have a hydrophobic domain. (I) have immunosuppressant, anti-HIV, neuroprotective, antianemic, vulnary, antitumor, osteopathic, anti-inflammatory and cytostatic activities, and can be used in gene therapy. (I) can be used as pharmaceuticals and as antigens to prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes for genetic diagnosis and gene sources for gene therapy or for producing (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals. Antibodies directed to (I) can be used for the detection, quantification and purification of proliferation/differentiation function, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activity/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity and anti-inflammatory activity. (I) and (II) can be used to treat autoimmune disorders e.g. multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis, inflammatory bowel disease and tumours. (I) and (II) can also be used for



DE Human single nucleotide polymorphism containing DNA sequence #640.  
XX  
KW Biallelic marker; polymorphism; human; disease; diagnosis; treatment;  
KW phenotypic trait; gene therapy; forensic; paternity; mapping; cancer;  
XX transgenic; single nucleotide polymorphism; SNP; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(59,A)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
PN W09953095-A2.  
XX  
PD 21-OCT-1999.  
XX  
PF 30-MAR-1999; 99WO-US006893.  
XX  
PR 09-APR-1998; 98US-00057871.  
XX  
PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
PI Lander ES, Wang D, Hudson T;  
DR WPI; 1999-620443/53.  
XX  
PT Polymorphic human genomic sequences and related allele-specific probes  
PT and primers, useful for genetic analysis, e.g. diagnosis and monitoring  
PT of disease.  
XX  
PS Claim 1; Page 99; 330pp; English.  
XX  
CC This invention describes novel human nucleic acid segments (I) containing  
CC polymorphic sites. The polymorphisms of (I) are used for, e.g.  
CC correlating disease polymorphisms (or disease susceptibility) or other  
CC phenotypic traits (e.g. baldness, obesity, fertility, strength, response  
CC to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation,  
CC heart or central nervous system diseases; detecting susceptibility to  
CC microbial infection; treating or preventing such diseases; forensic  
CC analysis; gene therapy; paternity testing; mapping genomic loci  
CC associated with phenotypic traits (and subsequent cloning of the genes  
CC responsible); and the production of transgenic organisms. Antibodies  
CC raised against (I) are useful as diagnostic and therapeutic tools and in  
CC drug screening. AAH85144 - AAH87644 represent the human DNA sequences  
CC containing biallelic polymorphic sites described in the invention  
XX  
SQ Sequence 133 BP; 25 A; 31 C; 43 G; 33 T; 0 U; 1 Other;  
  
Query Match 13.5%; Score 120.2; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 0;  
Matches 122; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 743 AAAACCGAGAGATAGCTGCTGTAGATAGCCGGCTTTCCATCCGGGATGTGGC 802  
DB 126 AAAACCGAGAGATAGCTGCTGTAGATAGCCGGCTTTCCATCCGGGATGTGGC 67  
QY ACACCTGCTACCAACCGAGATGTGGTATGAAACCCCTCTGATACGAAACCCCTTCTT 862  
DB 66 AACCTGCTACCAACCGAGATGTGGTATGAAACCCCTCTGATACGAAACCCCTTCTT 7  
QY 863 TTCCAA 868  
DB 6 TTCCAA 1  
  
RESULT 10  
ABT09032  
ID ABT09032 standard; DNA; 686 BP.  
XX  
AC ABT09032;  
XX  
DT 05-DEC-2002 (first entry)

XX  
DE Phase-1 Rat CT gene SEQ ID No 120.  
XX  
KW Rat; toxicity study; rat toxic response gene; toxicological response;  
KW drug development; phase-1 rat CT gene; dr.  
XX  
OS Rattus sp.  
XX  
PN W020026682-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 29-JAN-2002; 2002WO-US002935.  
XX  
PR 29-JAN-2001; 2001US-0264933P.  
XX  
PR 26-JUL-2001; 2001US-0308161P.  
XX  
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
XX  
PI Farris G, Hicken SH, Farr SB;  
XX  
DR WPI; 2002-674961/72.  
XX  
PT Evaluating the toxicity of an agent, useful in drug development or in  
PT determining toxicological responses to a new drug, by determining the  
PT expression of rat toxicologically relevant genes in the test animal in  
PT response to the test agent.  
XX  
PS Disclosure; Page 135; 388pp; English.  
XX  
CC The invention relates to a method used for evaluating the toxicity of an  
CC agent comprising determining the expression of a rat toxic response  
CC gene(s) in the test animal in response to the agent. The method is useful  
CC in drug development, particularly for conducting toxicity studies and  
CC analysis before a new drug or compound is approved for human consumption  
CC or use. The method is also useful in determining toxicological responses  
CC to a new drug. This polymorphic sequence represents a phase-1 rat CT  
XX  
SQ Sequence 686 BP; 159 A; 200 C; 203 G; 123 T; 0 U; 1 Other;  
  
Query Match 5.6%; Score 49.4001; DB 1; Length 686;  
Best Local Similarity 48.8%; Pred. No. 0;  
Matches 181; Conservative 0; Mismatches 166; Indels 24; Gaps 2;  
  
QY 355 CTATATCTGGTGTATGATGATCCAGATCCCTTACGACGACGACGACGAT 414  
DB 218 CTACACCTGTGTCTCTCAAGACCCCGATGCTCCGACGAGAGAGACCCCAATTCAAGGA 277  
QY 415 CTGAGACATTTGGCTGTAAACATATCAAGGCGCCGACCTGAAAGAAAGAAATTCA 474  
DB 278 GTGACACACCTTCTGTGTGTCAACATGAGGCAACGATATGACGTGGCACTGTCC- 336  
QY 475 GGGGCAAGATTTATACCTTACCAAGGCTCCCTCCCAACGCGACACAGTGGCTTCATCG 534  
DB 337 -----TCTCCGAATATCGTGGCTCCGACCTCCCAAGACACAGTGTGACCG 385  
QY 535 CTACAGTTCTTTGTCTATCTTCAAGAAAGAAAGATCATCTCTCTTCCAAAGAAA 594  
DB 386 CTAGTGTGCTGTGTATATGACGAGACGCTCTGAACTGTGACGAGCCATCTCTAG 445  
QY 595 CAAAATCT-----CGAGGCTTTGGAATAATGACAGATTTCTGAAACCGCTTCCA 642  
DB 446 CAACAGTCTGAGACAAACCGCGCAAGTTCAAGTGTGAGTCTCTTCGGAAGAAAGTACCA 505  
QY 643 CTTGGGCGAACCTGAAAGCAACCGACCGATTCATGACCCAGAACTTACAGACTTACCAAC 702  
DB 506 CTTGGAGCCCTCGGTGTGCGGACGTCTTCCAGGACAGTGGAGTACTGTGTGCCAA 565  
QY 703 CTTCCAGGCTC 713  
DB 566 GCTGATGATC 576



```

RESULT 11
AAd42238
ID AAd42238 standard; cDNA; 1078 BP.
XX
XX AAd42238;
AC
XX 04-NOV-2002 (first entry)
XX
XX Corn FT homologue cDNA #1.
DE
XX
XX Floral developmental protein; flowering locus T; APTALM3; transgenic;
XX FT; AP3; transgenic plant; fertility; flower development; gene mapping;
XX sterility; plant growth; inflorescence architecture; plant morphology;
XX tissue culture; cell division; corn; gene; ss.
XX
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
XX CDS 312..833
XX FT /*tag= a
XX FT /product= "Corn FT homologue protein"
XX
XX WO200244390-A2.
XX
XX 06-JUN-2002.
XX
XX 21-NOV-2001; 2001WO-US043750.
XX
XX 28-NOV-2000; 2000US-0253415P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
XX
XX WPI; 2002-547703/58.
XX
XX P-PSDB; AAE25736.
XX
XX New floral developmental polypeptide having flowering locus T or Ap3
XX homolog activity, useful for immunological screening of cDNA expression
XX libraries.
XX
XX Claim 6; Page 54; 88pp; English.
XX
XX The present invention relates to novel floral developmental proteins,
XX more specifically flowering locus T (FT) or APTALM3 (AP3) homologue
XX proteins and polynucleotides encoding such proteins. Floral developmental
XX polynucleotides are useful for transforming cells or for producing plants
XX by transforming the plant cells with the polynucleotides and regenerating
XX the plants from the transformed plant cells. Sequences of the invention
XX are useful for immunological screening of cDNA expression libraries. They
XX are also useful for creating transgenic plants. Polynucleotides of the
XX invention are used as probes for genetically and physically mapping the
XX genes that they are a part of and as markers for traits linked to those
XX genes. AP3 homologues may be useful for engineering plant sterility or
XX fertility, flower development and morphology. FT or TFL1 homologues are
XX useful for engineering flowering time, plant growth rate, inflorescence
XX architecture, tissue culture morphology and rate of cell division to
XX enhance transformation. The present sequence is corn FT homologue cDNA
XX from a contig of clones chn10.pk0052.f5, chn2.pk0035.f12,
XX cco1n.pk0010.h3, p0095.cwsa14f, p0119.cmtmg45rb and p0128.cpic142r
XX
XX Sequence 1078 BP; 197 A; 336 C; 321 G; 224 T; 0 U; 0 Other;
SQ
Query Match 5.5%; Score 48.8; DB 1; Length 1078;
Best Local Similarity 50.9%; Pred. No. 0;
Matches 138; Conservative 0; Mismatches 127; Indels 6; Gaps 1;
OY 182 CATTGAGCCCTCTTGAGACAGACACCCCTTTTGGCAGAGCCCTGAGTTTCTAACCA 241
DB 318 CATTGGAGATCCCGTGTGTGTGGCCGCATCATCGGGAGAGTGTGAGCCCTTCGTGCC 377
OY 242 GAGTTGGGAGACATTGGCTGCAAGGTTTCTGATTTGTAAACACTACAGAGAGATC 301

```

```

DB 378 CGGGTCCGCTCCGCGTGCCTACGCCCGCGAGGTCTCCMAAGGCTGCAAGCTCAGG 437
OY 302 ACCTCTGGATAG-----AGCCGATAGTCAAGTCCCGGGGGCCGTGAGACGCGCAACC 355
DB 438 CCTTCGCCATCGCCGACCAAGCCGCGCTCGAGGTGCGGCGAGACCCGACATGCGACCTTC 497
OY 356 TATATCTGTGTGATGTGATTCAGATGCCCTTACAGAGAGAAACCAAGACAGATTTC 415
DB 498 TACACCTCGTGTGATGTGATCTGTATCGCGGAGCCCGAGGATCCCAACTCAGGGAG 557
OY 416 TGAAGACATTGGCTGTGTAACAGATTCAGG 446
DB 558 TACCTGCACTGCTGTGATCTGATATTCGG 588

RESULT 12
AAd42243
ID AAd42243 standard; cDNA; 1191 BP.
XX
XX AAd42243;
AC
XX 04-NOV-2002 (first entry)
XX
XX Corn FT homologue cDNA from clone p0081.chcad07r.
XX
XX
XX Floral developmental protein; flowering locus T; APTALM3; transgenic;
XX FT; AP3; transgenic plant; fertility; flower development; gene mapping;
XX sterility; plant growth; inflorescence architecture; plant morphology;
XX tissue culture; cell division; corn; gene; ss.
XX
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
XX CDS 175..708
XX FT /*tag= a
XX FT /product= "Corn FT homologue protein"
XX
XX WO200244390-A2.
XX
XX 06-JUN-2002.
XX
XX 21-NOV-2001; 2001WO-US043750.
XX
XX 28-NOV-2000; 2000US-0253415P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
XX
XX WPI; 2002-547703/58.
XX
XX P-PSDB; AAE25741.
XX
XX New floral developmental polypeptide having flowering locus T or Ap3
XX homolog activity, useful for immunological screening of cDNA expression
XX libraries.
XX
XX Claim 6; Page 60; 88pp; English.
XX
XX The present invention relates to novel floral developmental proteins,
XX more specifically flowering locus T (FT) or APTALM3 (AP3) homologue
XX proteins and polynucleotides encoding such proteins. Floral developmental
XX polynucleotides are useful for transforming cells or for producing plants
XX by transforming the plant cells with the polynucleotides and regenerating
XX the plants from the transformed plant cells. Sequences of the invention
XX are useful for immunological screening of cDNA expression libraries. They
XX are also useful for creating transgenic plants. Polynucleotides of the
XX invention are used as probes for genetically and physically mapping the
XX genes that they are a part of and as markers for traits linked to those
XX genes. AP3 homologues may be useful for engineering plant sterility or
XX fertility, flower development and morphology. FT or TFL1 homologues are
XX useful for engineering flowering time, plant growth rate, inflorescence
XX architecture, tissue culture morphology and rate of cell division to

```

CC enhance transformation. The present sequence is corn FT homologue cDNA  
XX  
SQ Sequence 1191 BP; 280 A; 317 C; 344 G; 250 T; 0 U; 0 Other;  
Query Match 5.4%; Score 48.2; DB 1; Length 1191;  
Best Local Similarity 60.2%; Pred. No. 0;  
Matches 80; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
QY 315 AGCCGATAGTCAAGTTCCCGGGGCGCGTGGACCGCCCAACCTATATCTGTGATGTGG 374  
Db 326 AGCCGAGGATCGAGGTGCGGGGACCTGACATGAGACCTTCTACACCTCGTATGTGG 385  
QY 375 ATCCAGATGCCCTTAGCAGAGCAAAACCAACAGAGATTCTGGAGCAATTGGCTGTAA 434  
Db 386 ACCCGATGCTCGAGGCCAAGCGACCCGAACCTTAGGGAGTACTACACTGGCTGTGA 445  
QY 435 CAGATATCAAGG 447  
Db 446 CGGATATTCGGG 458

Search completed: February 22, 2005, 12:43:20  
Job time : 3 secs

```

/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ Hillman, Jennifer
/ Corley, Neil
/ Shah, Puri
/ TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/879,401
/ FILING DATE: 11-Jun-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/958,820
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0379 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 903 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: LONGTUT12
/ CLONE: 3126479
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-879-401-4

```

```

Query Match          96.5%; Score 858.9; DB 1; Length 903;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```

```

QY 2 AGTACTGTGTCCGGGTGTGACTGATTAAGTCTGCGAGACCTGGAACTGCTGCT 61
DB 1 AGTACTGTGTCCGGGTGTGACTGATTAAGTCTGCGAGACCTGGAACTGCTGCT 60
QY 62 TCTCCCTGTGCTTAACCAAGGTGCCGATAGGTTGACAATGAGGCTGTCAAGCAGA 121
DB 61 TCTCCCTGTGCTTAACCAAGGTGCCGATAGGTTGACAATGAGGCTGTCAAGCAGA 120
QY 122 CTGTATCTGGGTCTCATGATGTGCTCACTGAGACGAGAGTGAAGAACCCCGTGTGCC 181
DB 121 CTGTATCTGGGTCTCATGATGTGCTCACTGAGACGAGAGTGAAGAACCCCGTGTGCC 180
QY 182 CATGAGGCCCTCTTGGACGAGACACCTCTTTTGGCAGGGCCTTGAAGTTTCTAACCA 241
DB 181 CATGAGGCCCTCTTGGACGAGACACCTCTTTTGGCAGGGCCTTGAAGTTTCTAACCA 240
QY 242 GAGTTGGGGAACAATTGGCTGCAAGGTTGTCTGATTTGTAACAACAAGAAAGATC 301
DB 241 GAGTTGGGGAACAATTGGCTGCAAGGTTGTCTGATTTGTAACAACAAGAAAGATC 300
QY 302 AACTCTGATGAGAGCGGATGACAGTCCCGGGGGCGGTGAGCGGCGCAACTATATC 361
DB 301 AACTCTGATGAGAGCGGATGACAGTCCCGGGGGCGGTGAGCGGCGCAACTATATC 360

```

```

QY 362 CTGTGATGATGTGATTCAGATGCCCCCTTAGCAGACGAAACCAGACAGATTTCTGAGA 421
DB 361 CTGTGATGATGTGATTCAGATGCCCCCTTAGCAGACGAAACCAGACAGATTTCTGAGA 420
QY 422 CATTGGCTGTAAACAGATATCAAGGCGCCGACCTGAAAGAAAGGAAGATTCAAGGCCAG 481
DB 421 CATTGGCTGTAAACAGATATCAAGGCGCCGACCTGAAAGAAAGGAAGATTCAAGGCCAG 480
QY 482 GAGTTATAGCCTACCAAGCTCCCTCCCAACGGGACACAGTGGCTTCATCGTACAG 541
DB 481 GAGTTATAGCCTACCAAGCTCCCTCCCAACGGGACACAGTGGCTTCATCGTACAG 540
QY 542 TTCTTTGTCTATCTTCAGAAAGAAAGTCAATCTCTCTCTCCCAAGAAACAAACT 601
DB 541 TTCTTTGTCTATCTTCAGAAAGAAAGTCAATCTCTCTCTCCCAAGAAACAAACT 600
QY 602 CGAGGCTTTGAAAGTGAAGATTTGTGAACCGCTTCCACCTGGGGGAACTTGAAACA 661
DB 601 CGAGGCTTTGAAAGTGAAGATTTGTGAACCGCTTCCACCTGGGGGAACTTGAAACA 660
QY 662 AGCACCAGTTCAATGACCCAGAACTACCAAGGACTCACCAACCTCCAGGCTCCAGAGGA 721
DB 661 AGCACCAGTTCAATGACCCAGAACTACCAAGGACTCACCAACCTCCAGGCTCCAGAGGA 720
QY 722 AGGCGCAAGCGCCCAAGCACTAAACCAAGGCTAGATTTGTGCTGCTGCTGCTGCTGCT 780
DB 721 AGGCGCAAGCGCCCAAGCACTAAACCAAGGCTAGATTTGTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TTTGGCATCCGGGGCATGTGGCCACACTGCTTACCAACGACGATGTGGGTATGAAACCCCC 840
DB 781 TTTGGCATCCGGGGCATGTGGCCACACTGCTTACCAACGACGATGTGGGTATGAAACCCCC 840
QY 841 TCTGATACAGAACCCCTTCTTTTCCAAATTAACAAAAA 880
DB 841 TCTGATACAGAACCCCTTCTTTTCCAAATTAACAAAAA 880

```

Search completed: February 22, 2005, 12:49:27  
Job time : 1 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 12:49:26 ; Search time 1 Seconds

(without alignments)  
3.266 Million cell updates/sec

Title: US-10-035-958-60

Perfect score: 890

Sequence: 1 AAGTACTGTGTCTCCGGGTGG.....TAAAAAATCATCAAA 890

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 0.5

Searched: 2 seqs, 1835 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 2 summaries

Database: K035rnpb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	865.7	97.3	932	1	US-10-003-152-1
2	858.9	96.5	903	1	US-09-879-401-4

ALIGNMENTS

RESULT 1  
US-10-003-152-1  
; Sequence 1, Application US/10003152  
; Publication No. US20020151494A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkels, Richard  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Vernet, Corine  
; APPLICANT: Yang, Meijia  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Hermann, John  
; TITLE OF INVENTION: No. US20020151494A1 Amino Acid Sequences for Human Semaphorin-1  
; FILE REFERENCE: 15966-554 Cuz-54 CON-S12  
; CURRENT APPLICATION NUMBER: US/10/003,152  
; PRIOR FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: 09/604,286  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/140,584  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 932  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

NAME/KEY: CDS  
LOCATION: (113)...(793)  
US-10-003-152-1

Query Match 97.3%; Score 865.7; DB 1; Length 932;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 881; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY	1	AAGTACTGTGTCTCCGGGTGGACTGATTAAGTCCGAGCCCTGGAAGCTGCTGTCC	60
DB	25	AAGTACTGTGTCTCCGGGTGGACTGATTAAGTCCGAGCCCTGGAAGCTGCTGTCC	84
QY	61	TTCTCCCTGTGTCTTAACAGAGTCCCATGAGTGTGAACAATGAGCTGTGACAGCAG	120
DB	85	TTCTCCCTGTGTCTTAACAGAGTCCCATGAGTGTGAACAATGAGCTGTGACAGCAG	144
QY	121	ACTGTTAAGTGTCTCATGATGTGTGCTCATGAGACGAGATGAAACACCCGTGTGC	180
DB	145	ACTGTTAAGTGTCTCATGATGTGTGCTCATGAGACGAGATGAAACACCCGTGTGC	204
QY	181	CCATGAGGCCCTCTTGAAGAGACACCCCTTTTTCAGAGGCTTGAAGTTTCTACCC	240
DB	205	CCATGAGGCCCTCTTGAAGAGACACCCCTTTTTCAGAGGCTTGAAGTTTCTACCC	264
QY	241	AGAGTTGGGAAACATTGGCTCAAGTGTCTCTGATTGTAACTACAGACAGAAAT	300
DB	265	AGAGTTGGGAAACATTGGCTCAAGTGTCTCTGATTGTAACTACAGACAGAAAT	324
QY	301	CACCTCTGTGATGAGACCGATATGTAAGTTCCCGGGGCGGTGAGCGGCGCACTATAT	360
DB	325	CACCTCTGTGATGAGACCGATATGTAAGTTCCCGGGGCGGTGAGCGGCGCACTATAT	384
QY	361	CCTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420
DB	385	CCTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	444
QY	421	ACATTGGCTGTGTAACAGATTAACAGAGGCGCGACCTTGAAGAAAGGAATTCAGAGCCA	480
DB	445	ACATTGGCTGTGTAACAGATTAACAGAGGCGCGACCTTGAAGAAAGGAATTCAGAGCCA	504
QY	481	GAGATTAACAGGCTTACAGAGGCTTCCCTCCAGCCGAGCAACAGTGGCTTCCATGACCA	540
DB	505	GAGATTAACAGGCTTACAGAGGCTTCCCTCCAGCCGAGCAACAGTGGCTTCCATGACCA	564
QY	541	GTCTTTGTCTATCTTCAAGAAAGAAAGTATCTCTCTCTCCCAAGAAACAAAC	600
DB	565	GTCTTTGTCTATCTTCAAGAAAGAAAGTATCTCTCTCTCCCAAGAAACAAAC	624
QY	601	TCGAGGCTCTTGGAAAATGAGAGATTTGAAACCCCTTCCACCTGGGCGAACCTGAAGC	660
DB	625	TCGAGGCTCTTGGAAAATGAGAGATTTGAAACCCCTTCCACCTGGGCGAACCTGAAGC	684
QY	661	AAGCAACCAATTATGACCCAGAACTAACAGAGCTAACCAACCTTCCAGGCTCCAGAGA	720
DB	685	AAGCAACCAATTATGACCCAGAACTAACAGAGCTAACCAACCTTCCAGGCTCCAGAGA	744
QY	721	AAGGCGCAGGAGCCCAAGAC-AAAACAGAGAGATAGTCTCTGTAGATAGCCG	779
DB	745	AAGGCGCAGGAGCCCAAGAC-AAAACAGAGAGATAGTCTCTGTAGATAGCCG	804
QY	780	CTTTGCAATCCGGGCAATGTGCGCACCTGTACACCGACGATGTGGATATGAACCC	839
DB	805	CTTTGCAATCCGGGCAATGTGCGCACCTGTACACCGACGATGTGGATATGAACCC	864
QY	840	CTCTGATACAGAACCCCTTCTTTTCAAAATTAATAATATCAAA 889	
DB	865	CTCTGATACAGAACCCCTTCTTTTCAAAATTAATAATATCAAA 914	

RESULT 2  
US-09-879-401-4  
; Sequence 4, Application US/09879401  
; Publication No. US20030119730A1

Primer A: TTGGAAGAAGGGGTTCTG  
Primer B: AAGCACAAAACGAGCG  
STS size: 133  
PCR profile:

This Page Blank (uspto)

```

QY 181 CCATGAGGCCCTCTTGGACGAGCACCCCTCTTTTCCAGGCGCTTGAAGTTTCTACCC 240
Db 192 CCATGAGGCCCTCTTGGACGAGCACCCCTCTTTTCCAGGCGCTTGAAGTTTCTACCC 251
QY 241 AGAGTTGGGGAACATTTGGCTCGAAGTTTGTCTGATTTGAACAACACTACAGAGAAGAT 300
Db 252 AGAGTTGGGGAACATTTGGCTCGAAGTTTGTCTGATTTGAACAACACTACAGAGAAGAT 311
QY 301 CACTCTCTGGATGGAGCCGATAGTCAAGTTCCCGGGGCGGTGACGCGCAACTATAT 360
Db 312 CACTCTCTGGATGGAGCCGATAGTCAAGTTCCCGGGGCGGTGACGCGCAACTATAT 371
QY 361 CCTGGTATGATGATCCAGATGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
Db 372 CCTGGTATGATGATCCAGATGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 431
QY 421 ACATTGGCTGTAAACAGATATCAGAGGCGCGACCTGAAAGAGGAGATTTCAGGGCCA 480
Db 432 ACATTGGCTGTAAACAGATATCAGAGGCGCGACCTGAAAGAGGAGATTTCAGGGCCA 491
QY 481 GAGTTATACGCTTACAGGCTCCCTCCACCGGCACACAGTGGCTTCCATGCTACCA 540
Db 492 GAGTTATACGCTTACAGGCTCCCTCCACCGGCACACAGTGGCTTCCATGCTACCA 551
QY 541 GTTCTTTGTCTATCTTTCAGAGGAAAGTATCTCTCTCTTCCCAAGGAAACAAAC 600
Db 552 GTTCTTTGTCTATCTTTCAGAGGAAAGTATCTCTCTCTTCCCAAGGAAACAAAC 611
QY 601 TCAGAGCTCTTGGAAATGACAGATTCTGAACCGCTTCCACTGGGCGAACCCTGAAGC 660
Db 612 TCAGAGCTCTTGGAAATGACAGATTCTGAACCGCTTCCACTGGGCGAACCCTGAAGC 671
QY 661 AAGCACCAGTTTCATGACCCAGAACTACAGGAGTCAACCAACCTCCAGGCTCCAGAGG 720
Db 672 AAGCACCAGTTTCATGACCCAGAACTACAGGAGTCAACCAACCTCCAGGCTCCAGAGG 731
QY 721 AAGGCGCAGGAGCCCAAGCAC-AAACCCAGGACAGATAGTCTGCTAGATAGCCGG 779
Db 732 AAGGCGCAGGAGCCCAAGCACAAACCCAGGCGGAGATAGTCTGCTAGATAGCCGG 791
QY 780 CTTTCCATCCCGGATGCGGCACACTGCTCACCACCGCATGATGGATGGAAACCC 839
Db 792 CTTTCCATCCCGGATGCGGCACACTGCTCACCACCGCATGATGGATGGAAACCC 851
QY 840 CTTGGATACAGAACCCCTCTTTTCCAAATTAATAAATAATCATCA 889
Db 852 CTTGGATACAGAACCCCTCTTTTCCAAATTAATAAATAATCATCA 901

```

## RESULT 2

AAA15582  
ID AAA15582 standard; cDNA, 903 BP.

XX  
AC AAA15582;

DT 01-AUG-2000 (first entry)

DE Human phospholipid binding protein 2, PLBP2 gene.

XX Human; phospholipid binding protein; PLBP2; foetal development disorder;  
XX reproduction disorder; cell proliferation disorder; immune response;  
XX autoimmune disorder; AIDS; infertility; cytoskeletal; immunosuppressive;  
XX gene therapy; hereditary neuropathy;  
XX phosphatidylethanolamine binding protein D1; PE-BP D1; ss.

XX Homo sapiens.

Key Location/Qualifiers  
CDS 88..771  
/\*tag= a  
/product= "Human PLBP2"

PN US063767-A.

XX  
PD 16-MAY-2000.

XX 09-DEC-1998; 98US-00208718.

XX 28-OCT-1997; 97US-00958820.

XX (INCY-) INCYTE PHARM INC.

XX Corley NC, Shah P, Lal P, Hillman JL;

XX WPI; 2000-375529/32.

XX P-PSDB; AAY94263.

XX New purified phospholipid binding proteins 1 and 2 useful for diagnosing,  
XX treating or preventing diseases disorders associated with fetal  
XX development, reproduction, cell proliferation, and the immune response.  
XX Example 5; Fig 2; 37pp; English.

XX The present sequence is the phospholipid binding protein 2 (PLBP2) gene.  
XX This gene is expressed in lung, prostate and heart tissues. Also, the  
XX protein is expressed in foetal tumour tissues. PLBP2 may be used for the  
XX diagnosis, prevention, or treatment of disorders associated with foetal  
XX development (e.g. hereditary neuropathies), reproduction (e.g.  
XX infertility), cell proliferation (e.g. cancer), and the immune response  
XX (AIDS). PLBP2 antibodies may also be developed for potential drug  
XX screening or to quantitate PLBP2 gene expression in biopsied tissues. The  
XX PLBP2 gene may be administered for gene therapy of disorders associated  
XX with PLBP2. PLBP2 has high homology with the phosphatidylethanolamine  
XX binding protein D1, PE-BP D1, of Onchocerca volvulus. PE-BP D1 is thought  
XX to play a role in transport or signal mechanisms between membranes and  
XX the cytoplasm

XX Sequence 903 BP; 222 A; 251 C; 242 G; 188 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 96.5%; Score 858.9; DB 1; Length 903;

Matches 873; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY	2	AGTACTTGTGTCGGGTGGTGGACTGGATTAGCTGCGAGCCCTGGAGCTGCCTGCTCT	61
Db	1	AGTACTTGTGTCGGGTGGTGGACTGGATTAGCTGCGAGCCCTGGAGCTGCCTGCTCT	60
QY	62	TCTCCCTGTGCTTAACAGAGGTGCCCATGGTTGGACAATGAGGCTGGTCAACAGCAGCA	121
Db	61	TCTCCCTGTGCTTAACAGAGGTGCCCATGGTTGGACAATGAGGCTGGTCAACAGCAGCA	120
QY	122	CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGACGCGCTGTGTC	181
Db	121	CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGACGCGCTGTGTC	180
QY	182	CATGAGGCCCTCTTGGACGAGGACACCTCTTTTCCAGGCGCTTGAAGTTTCTACCCA	241
Db	181	CATGAGGCCCTCTTGGACGAGGACACCTCTTTTCCAGGCGCTTGAAGTTTCTACCCA	240
QY	242	GAGTTGGGGAACATTGGCTCAAGGTTGTCCTGATTTGAACAACACTACAGAGAAGATC	301
Db	241	GAGTTGGGGAACATTGGCTCAAGGTTGTCCTGATTTGAACAACACTACAGAGAAGATC	300
QY	302	ACCTCTCTGATGAGCGCGATAGTCAAGTTTCCCGGGGCGGTGACGCGCGCAACTATATC	361
Db	301	ACCTCTCTGATGAGCGCGATAGTCAAGTTTCCCGGGGCGGTGACGCGCGCAACTATATC	360
QY	362	CTGGTATGGTGGATCCAGATGCCCTTAGCAGACGAGAACCCAGACAGAGATTCTCGAGA	421
Db	361	CTGGTATGGTGGATCCAGATGCCCTTAGCAGACGAGAACCCAGACAGAGATTCTCGAGA	420
QY	422	CATTGGCTGTAAACAGATATCAGGGCGCGACTTGAAGAGAGGGAAGATTTCAGGGCCAG	481
Db	421	CATTGGCTGTAAACAGATATCAGGGCGCGACTTGAAGAGAGGGAAGATTTCAGGGCCAG	480

This Page Blank (uspto)





This Page Blank (uspto)